Figure 1A

1	CCCACGCGTCCGATTAAAGTGAGGAGAGAGCTACAACCAAGTAAGCAAGTGTCAGGGCTC	60
61 1	ACCAACCATGCAAGGACAGGGGGAGAAGAGAGACATATTTTGTTCCAA M O G O G R R R G T C K D I F C S K	120 18
121 19	AATGGCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTG	180 38
181 39	TGTGTCCCCGGCCAATGCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCC V S P A N A P S A Y P R P S S T K S T P	240 58
2 4 1 59	TGCCTCACAGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGT ASQVYSLNTDFAFRLYRRLV	300 78
301 79		360 98
361 99		420 118
421 119	CAACCTCACACACACACAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTC N L T H T P E S A I H Q G F Q H L V H S	480 138
481 139		540 158
541 159		600 178
601 179	CTTTTCTACAGATTTCTCCAACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAA F S T D F S N P S I A Q A R I N S H V K	660 198
661 199		720 218
721 219		780 238
781 239	TACAAGAAAGAACTTCCCATTCCTGGTGGGCGAGCAGGTCACTGTGCAAGTCCCCATGAT T R K N F P F L V G E Q V T V Q V P M M	840 258
841 259		900 278

Figure 1B

901 279	GATGGATTACAAGGGAGATGCCGTGGCCTTCTTTGTCCTCCCTAGCAAGGGCAAGATGAG M D Y K G D A V A F F V L P S K G K M R	960 298
213		250
961	GCAACTGGAACAGGCCTTGTCAGCCAGAACACTGATAAAGTGGAGCCACTCACT	1020
299	Q L E Q A L S A R T L I K W S H S L Q K	318
1021		1080
319	RWIEVFIPRFSISASYNLET	338
1081	CATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGACAAAAATGCTGATTTTTCTGGAAT	1140
339	I L P K M G I Q N A F D K N A D F S G I	358
1141	TGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCCACAAGGCTGTGCTGGATGTCAG	1200
359	A K R D S L Q V S K A T H K A V L D V S	378
1201	TGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAGTTCATAGTCCGATCGAAGGA	1260
379	E E G T E <u>A T A A</u> T T T K F I V R S K D	398
1261	TGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCTGATGATGATTACAAATAA	1320
399	GPSYFTVSFNRFTVM TNK	418
1321 419	AGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATCCCACTAAAATCCTAGGTGGGAAAATTCCTAGGTGGGAAAAATCCCACTAAAATCCTAGGTGGGAAAATTCCTAGGTGGGAAAATTCCTAGGTGGGAAAATTCCTAAATTCCTAGGTGGGAAAATTCCTAGGTGGGAAAATTCCTAGGTGGGAAAATTCCTAGGTGGGAAAATTCCTAAATTCTAGGTGGGAAAATTCCTAGGTGGGAAAATTCCTAGGTGGGGAAAATTCCTAAATTCTAGGTGGGAAAATTCCTAGGTGGGGGAAAATTCCTAGATATAATATGTGAAATTCCTAGGTGGGAAAATTCCTAGGTGGGAAAATTCCTAGATATATAT	1380 436
1381	AAATGGCCTGTTAACTGATGGCACATTGCTAATGCACAAGAAATAACAAACCACATCCCT	1440
1441	CTTTCTGTTCTGAGGGTGCATTTGACCCCAGTGGAGCTGGATTCGCTGGCAGGGATGCCA	1500
1501		1560
1561	AACCCCAGTCAGTGCCCTTTTCCACAAATTCTCCCCAGGTAACTAGCTTCATGGGATGTTG	1620
1621		1680
1681	TAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAAACTAAAATATGAAAAAAAA	1740
1741	AAAAAAAAAAAAAAAAAAAAAA 1766	

Figure 2

AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(1) (1) (1) (1)	1 50 MQGQGRRRGTCKDIFCSKMASYLYGVTFAVGLCAPIYCVSPANAPSAYPRMERMLPTLALGTLAAGFCPAVLCHPNSPLDMHLIDYLLTLLVGTLALSHGQLHVEHDGESCSMSPFLYLVTLVLGTHATIHCASPEGKVTACHS
AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(51) (31) (33) (33)	51 100 PSSTKSTPASQVYSLNTDFAFRLYRRLVLETFSQNIFFSPVSV EENLTQENQDRGTHVDLGLASANVDFAFSLYKQLVLKAPDKNVIFSPLSI NSSHQQILETGEGSPSLKIAPANADFAFRFYYLIASETFGKNIFFSPLSISQPNATLYKMSSINADFAFNLYRRFTVETPDKNIFFSPVSI
AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(94) (81) (83) (74)	101 150 STSLAMLSLGAHSVTKTQTLQGLGFNLTHTPESAIHQGFQHLVHSLTVPS STALAFLSLGAHNTTLTETLKGLKFNLTETSEAEIHQSFQHLLRTLNQSS SAAYAMLSLGACSHSRSQTLEGLGFNLTELSESDVHRGFQHLLHTLNLPG SAALVMLSFGACCSTQTETVETLGFNLTDTPMVEIQHGFQHLICSLNFPK
AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(144) (131) (133) (124)	151 200 KDITLKMGSÄLFVKKEI QLQANFLGNVKRLYEAEVFSTDFSNPSIAQARI DEI QLSMGNÄMFVKEQISLLDRFTEDAKRLYGSEAFAIDFQDSAAAKKLI HGI ETRVGSÄLFLSHNIKFLAKFLNDTMAVYEAKLEHTNFYDTVGTIQLI KEI ELQIGNÄLFIGKHIKPLAKFLNDVKTLYETEVFSTDFSNISAAKQEI
AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(194) (181) (183) (174)	250 NSHVKKKTQGKVVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNF NDYVKNGTRGKITDLIKDLDSQTMMVLVNYIFFKAKWEMPFDPQDIHQSR NDHVKKETRGKIVDLVSELKKDVLMVLVNYIYFKALWEKPFISSRTTPKD NSHVEMQTKGKVVGLIQDLKPNTIMVLVNYIHFKAQWANPFDPSKTEDSS
AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(244) (231) (233) (224)	300 PFLVGEQVTVQVPMMHQKEQFAFGVDTELNCFVLQMDYKGDAVAFFVLPS FYLSKKKWVMVPMMSLHHLTIPYFRDEELSGTVVELKYTGNASALFILPD FYVDENTTVRVPMMLQDQEHHWYLHDRYLPGSVLRMDYKGDATVFFILPN SFLIDKTTTVQVPMMHQMEQYYHLVDMEINGTVLQMDYSKNALALFVLPK
AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(294) (281) (283) (274)	301 350 KGKMRQLEQALSARTIIKWSHSLQKRWIEVFIPRFSISASYNLETI QDKMEEVEAMLLPETIKRWRDSLEFREIGELYLPKFSISRDYNUNDI QGKMREIEEVLTPEMLMRWNNLLRKRNFYKKLELHLPKFSISGSYVLDQI EGQMESVEAAMSSKTLKKWNRLLQKGWVDLFVPKFSISATYDLGAT
AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(340) (328) (333) (320)	351 400 LPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT LLQLGIEEAFTSKADLSGITGARNLAVSQVVHKAVLDVFEEGTEASAATA LPRLGFTDLFSKWADLSGITKQQKLEASKSFHKATLDVDEAGTEAAAATT LLKMGIQHAYSENADFSGLTEDNGLKLSNAAHKAVLHIGEKGTEAAAVPE
AL132708_FL AACT_HUMAN KAIN_HUMAN THBG_HUMAN	(390) (378) (383) (370)	401 \$\frac{\dagger}{\dagger}\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\dagger\d

Figure 3

LSI-01 pdb1q1p	MQGQGRRRGT	CKDIFCSKMA	SYLYGVLFAV		PANAPSAYPR GDAAQKTDTS
LSI-01 pdb1q1p		45,000,000	FRLYRRLVLE FSLYRQLAHQ	1 (0006) (COC) - COC) 1	VSVSTSLAML VSIATAFAMI
LSI-01 pdb1q1p	BC 50 50000 ED 3	ETTEGENENT ÖTTÖGTGENE	THTPESATHQ TEIPEAQTHE	GFQHLVHSLT GFQELLRTLN	888 BO FO
LSI-01 pdb1q1p			KRLYEAEVFS KKLYHSEAFT		
LSI-01 pdb1q1p	E. 2007 (1990)	E000.003 6008 6008	VNHIFFKAKW VNYIFFKGKW	\$20\$ becauses	608 808 -
LSI-01 pdblqlp			ELNCFVLQMD KLSSWVLLMK		
LSI-01 pdb1q1p			IEVFIERFSI ASLHLEKLSI		
LSI-01 pdb1q1p	Marie Contra		HKAVL <mark>DVSEE</mark> HKAVLTIDEK	GTEATAATTT GTEAAGAMFL	
LSI-01 pdb1q1p	B00 B00 B0	TFLMMITNKA PFVFLMIEQN		enptks Vnptqk	

Figure 4.

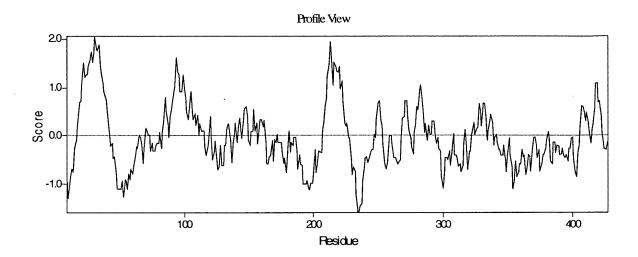
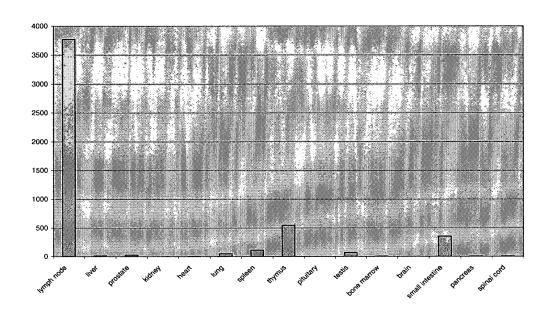


Figure 5.



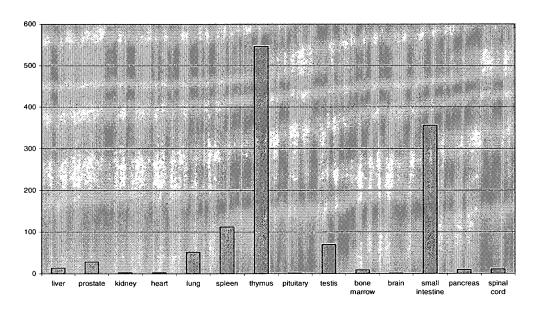


Figure 6.

Protein	Genbank ID	<u>Identities</u>	<u>Similarities</u>
human α ₁ -antichymotrypsin	gil112874	46%	52%
human Kallistatin	gil5453888	48%	56%
human thyroxin-binding	gil37142	51%	57%
globulin human (aantithrypsin	gil6137432	43%	50%

Figure 7

